TECH CENTER 1600/2900   APR 2 5 2002   RECEIVED

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _09/689,343A_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino Numbering

The numbering under each 5° amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ✓ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _4_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

BIOTECHNOLOGY
SYSTEMS
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RAW SEQUENCE LISTING
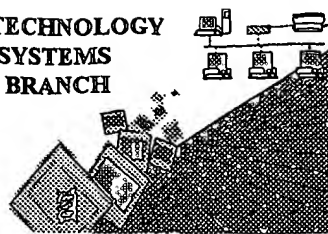## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _09/689,343A_
Source: _/600_
Date Processed by STIC: _4/16/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/689,343A   TIME: 11:52:53

Input Set : A:\NEB-181.txt
Output Set: N:\CRF3\04162002\I689343A.raw

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 3 <110> APPLICANT: VAISVILA, ROMUALDAS
 4         MORGAN, RICHARD D.
 5         KUCERA, REBECCA B.
 6         CLAUS, TOBY E.
 7         RALEIGH, ELISABETH A.
 9 <120> TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
10         ENDONUCLEASE
12 <130> FILE REFERENCE: NEB-181
14 <140> CURRENT APPLICATION NUMBER: 09/689,343A
15 <141> CURRENT FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 903
23 <212> TYPE: DNA
24 <213> ORGANISM: Micrococcus sp.
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(900)
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35 gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc      96
36 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
37              20                  25                  30
39 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg     144
40 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
41          35                  40                  45
43 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc     192
44 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
45      50                  55                  60
47 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat     240
48 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
49  65                  70                  75                  80
51 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg     288
52 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
53              85                  90                  95
55 gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg     336
56 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
57             100                 105                 110
59 gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc     384
60 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
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63  gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc    432
64  Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
65      130       ·       .            135                    140
67  gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg    480
68  Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
69  145                   150                    155                160
71  tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat    528
72  Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
73                  165       .            170                   175
75  cgc gag ccc tac atg.gcg ccc ggg ctc gtt aca ccc gag aag gta gcg    576
76  Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
77              180                    185                    190
79  ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct    624
80  Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
81          195                    200                    205
83  gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc    672
84  Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
85      210                    215                    220
87  atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg    720
88  Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
89  225                   230                    235                240
91  gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc    768
92  Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
93                  245                    250                    255
95  gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta    816
96  Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
97              260                    265                    270
99  atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc    864
100 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
101         275                    280                    285
103 gtg cag act ccc cag agt gac cca cga acc gac gga tga                 903
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109 <211> LENGTH: 300
110 <212> TYPE: PRT
111 <213> ORGANISM: Micrococcus sp.
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118             20                   25                   30  .
120 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
121         35                   40                   45  ·
123 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
124     50                   55                   60
126 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
127 65                   70                   75                   80
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129 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
130              85              90              95
132 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
133             100             105             110
135 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
136         115             120             125
138 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
139     130             135             140
141 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
142 145               . 150             155             160
144 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
145             165             170             175
147 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
148             180             185             190
150 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
151         195             200             205
153 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
154     210             215             220
156 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
157 225             230             235             240
159 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
160             245             250             255
162 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
163         260             265             270
165 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
166         275             280             285
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174 <212> TYPE: DNA
175 <213> ORGANISM: Unknown
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Unknown Organism: ENVIRONMENTAL DNA
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181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(1233)
184 <220> FEATURE:
185 <223> OTHER INFORMATION: At position 594, N = G, A, C or T
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189 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
190  1               5                  10                 15
192 acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg     96
193 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
194             20              25              30
196 cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg    144
197 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
198         35              40              45
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RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/689,343A   TIME: 11:52:53

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Output Set: N:\CRF3\04162002\I689343A.raw

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202     50                  55                  60
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205 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
206  65                  70                  75                  80
208 tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag   288
209 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
210                  85                  90                  95
212 tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta   336
213 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
214                  100                 105                 110
216 ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg   384
217 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
218             115                 120                 125
220 gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc   432
221 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
222     130                 135                 140
224 ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc   480
225 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
226 145                 150                 155                 160
228 tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt   528
229 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
230                  165                 170                 175
232 tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa   576
233 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
234                  180                 185                 190
236 cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc   624
237 Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
238             195                 200                 205
240 ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac   672
241 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
242 210                 215                 220
244 tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc   720
245 Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
246 225                 230                 235                 240
249 tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc   768
250 Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
251                  245                 250                 255
253 tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg   816
254 Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
255                  260                 265                 270
257 aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac   864
258 Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
259             275                 280                 285
261 gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc   912
262 Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
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W-Y-> 236
W-->   237

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270 Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
271             325             330             335
273 cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa   1056
274 Arg Leu Gln Ala Pro Phe Leu Val Asp Phe Trp Glu Val Asp Asp Gln
275             340             345             350
277 tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc   1104
278 Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
279             355             360             365
281 ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg   1152
282 Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
283     370             375             380
285 ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca   1200
286 Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
287 385             390             395             400
289 ggt cga gcc gat agc cct cac ccc gta tcg ttt tga                   1236
290 Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
291             405             410
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 411
296 <212> TYPE: PRT
297 <213> ORGANISM: (Unknown)
299 <220> FEATURE:
300 <223> OTHER INFORMATION: At position 198, Xaa = any amino acid
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307             20             25             30
309 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
310             35             40             45
312 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
313     50             55             60
315 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
316 65             70             75             80
318 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
319             85             90             95
321 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
322             100             105             110
324 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
325     115             120             125
327 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
328     130             135             140
330 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
331 145             150             155             160
333 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
334             165             170             175
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handwritten: See item 6 on Erra Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/16/2002
PATENT APPLICATION: US/09/689,343A   TIME: 11:52:54

Input Set : A:\NEB-181.txt
Output Set: N:\CRF3\04162002\I689343A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 594
Seq#:3; Xaa Pos. 198
Seq#:4; Xaa Pos. 198

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:6   another error